

<!--StartFragment-->RESULT 7
PCT-US02-22833-26
; Sequence 26, Application PC/TUS0222833
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti G.
; APPLICANT: HONNCHELL, Cynthia D.
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: TANG, Y. Tom
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: BARROSO, Ines
; APPLICANT: YUE, Henry
; APPLICANT: WARREN, Bridget A.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: AZIMZAI, Yalda
; APPLICANT: LEE, Ernestine A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: GORVAD, Ann E.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: TRAN, Bao
; APPLICANT: LI, Joana X.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: ZEBARJADIAN, Yeganeh
; APPLICANT: TRAN, Uyen K.
; APPLICANT: YAO, Monique G.
; APPLICANT: PETERSON, David P.
; APPLICANT: LUO, Wen
; APPLICANT: LEHR-MASON, Patricia M.
; TITLE OF INVENTION: RECEPTORS AND MEMBRANE ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1082 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/22833
; CURRENT FILING DATE: 2002-07-16
; PRIOR APPLICATION NUMBER: US 60/306,020
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/308,179
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/309,702
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: US 60/311,476
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,718
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/311,551
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/314,798
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/316,639
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/317,996
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PERL Program
; SEQ ID NO 26
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

SEQ ID NO 26

PCT/US02/22833

; OTHER INFORMATION: Incyte ID No: 566361CB1
PCT-US02-22833-26

Query Match 78.7%; Score 1954.6; DB 1; Length 3320;
Best Local Similarity 87.7%; Pred. No. 0;
Matches 2186; Conservative 0; Mismatches 289; Indels 18; Gaps 4;

Qy	1 ATGGCCTCAGCTGACAAGAATGGCAGCAACCTCCCATCTGTGTCTGGTAGCCGCCTGCAG 60
Db	282 ATGGCCTCTGCTGACAAGAATGGCGGGAGCGTGTCCCTCTGTGTCCAGCAGCCGCCTGCAG 341
Qy	61 AGCCGGAAGCCACCCAACCTCTCCATCACCATCCGCCACC-----AGAGAGCCAGGCC 114
Db	342 AGCCGGAAGCCACCCAACCTCTCCATCACCATCCGCCACCCGAGAAAGAGACCCAGGCC 401
Qy	115 CCCGGCGAGCAGGATAGCATGTTCTGAGAGGGCGAAGAACCCAGCCTACCTGAAGAGT 174
Db	402 CCTGGCGAGCAGGACAGCATGCTGCCCTGAGAGG---AAGAACCCAGCCTACTTGAAGAGC 458
Qy	175 GTCAGCCTACAGGAGCCCCGGGACGATGGCAGGAGGGCGCAGAGAAGCGCCCCGGCTTC 234
Db	459 GTCAGCCTCCAGGAGCCACGCCAGCGATGGCAGGAGAGTTAGAGAAGCGCCCTGGCTTC 518
Qy	235 CGCCGCCAGGCCTCCCTGTCCAGAGCATCCGAAAGAGCACAGCCCAGTGGTTGGGTC 294
Db	519 CGCCGCCAGGCCTCACTGTCCAGAGCATCCGAAAGGGCGCAGCCCAGTGGTTGGAGTC 578
Qy	295 AGCGGCGACTGGGAGGGCAAGCGACAAAATGGCATCGTCGAGCCTGCACCACTGCAGC 354
Db	579 AGCGGCGACTGGGAGGGCAGCGGCAGCAGTGGCAGCGCCAGCCTGCACCACTGCAGC 638
Qy	355 GTGCACTATGGCCGCCTCAAGGCCTCGGCCAGAGAGAACTGGAGCTGCCAGCCAGGAG 414
Db	639 ATGCGCTACGGCCGCCTGAAGGCCTCGCCAGCGTACCTGGAGCTCCCAGCCAGGAG 698
Qy	415 GTGCCATCCTCCAGGGCACTGAGTCTCAAAACCGTCAAGATGCCAAGATTGTGGAT 474
Db	699 GCACCGTCCTCCAGGGCACTGAGTCCCCAAGCCCTGCAAGATGCCAAGATTGTGGAT 758
Qy	475 CCACTGGCTGGGTAGGGCCTCCGCCATCCAGATGAGGTGGACCGGCCCTCACGCTGCC 534
Db	759 CCGCTGGCCCGGGCCGGCCTCCGCCACCCGGAGGAGATGGACAGGCCACGCCCTG 818
Qy	535 CACCCACCTCTGACTCCAGGGGTCTGTCTCACATCCTCACCAAGTGTCCGCTCTGGC 594
Db	819 CACCCACCGCTGACCCCCGGAGTCCTGTCCCTCACCTCCTCACCAAGTGTCCGTTCTGGC 878
Qy	595 TACTCCCACATCTGCCCGCCGAAGAGGATATCTGTTGCCATATGAGCTTCAGGCAGCC 654
Db	879 TACTCCCACCTGCCACGCCGAAGAGAATGTCTGTGGCCACATGAGCTTGCAAGCTGCC 938
Qy	655 GCCGCCCTCCTCAAGGGCGTTCCGTGCTAGATGCGACTGGCAGCGGTGCCGGCATGTC 714
Db	939 GCTGCCCTCCTCAAGGGCGCTCGGTGCTGGATGCCACCGGACAGCGGTGCCGGTGGTC 998
Qy	715 AAACGCAGCTTCGCTTACCCAGCTTCTGGAGGAGGATGCTGCGATGGAGCTGACACC 774
Db	999 AAGCGCAGCTTGGCCTTCCCAGCTTCTGGAGGAGGATGTGGTCATGGGGCAGACACG 1058
Qy	775 TTGACTCCTCCTTTAGTAAGGAAGAAATGAGCTCCATGCCTGACGATGTCTTGAG 834

Db 1059 TTTGACTCCTCCTTTAGTAAGGAAGAAATGAGCTCCATGCCTGATGATGTCTTGAG 1118
 Qy 835 TCCCCCCCACACTCTGCCAGCTACTTCCGAGGTGTCACACTCTGCCTCCCCGGTCTCC 894
 Db 1119 TCCCCCCCACACTCTGCCAGCTACTTCCGAGGGATCCCACACTCAGCCTCCCTGTCCTCC 1178
 Qy 895 CCGGATGGAGTGCACATCCCGCTAAAAGAATAACAGCGGTGGCCGAGCCCTGGTCCCGGG 954
 Db 1179 CCCGATGGGTGCAAATCCCTCTGAAGGAGTA-----TGGCCGAGCCCCAGTCCCCGGG 1232
 Qy 955 ACCCAGCGTGGCAAACGCATTGCCTCAAAGTAAAGCACTTGCATTGACCGGAAGAAG 1014
 Db 1233 CCCCGGCGCGCAAGCGCATCGCCTCCAAGGTGAAGCACTTGCCTTGATCGGAAGAAG 1292
 Qy 1015 AGGCACTACGGCTGGGTGCTGGTAACCTGGCTCAACCAGAAGCTATCGACGCAGCATC 1074
 Db 1293 CGGCACTACGGCTCGGCGTGGTGGCAACTGGCTGAACCGCAGCTACCGCCGAGCATC 1352
 Qy 1075 AGCAGCACCGTGCAGCGGCAGCTGGAGAGCTTCGATAGCCACCGGCCACTTCACCTAC 1134
 Db 1353 AGCAGCACTGTGCAGCGGCAGCTGGAGAGCTTCGACAGCCACCGGCCACTTCACCTAC 1412
 Qy 1135 TGGCTGACGTTCGTTACATCATCATCACCTGCTGGTGTGCACCTATGGCATCGCA 1194
 Db 1413 TGGCTGACCTTCGTCATGTACATCACGCTGCTGGTGTGCACGTATGGCATCGCA 1472
 Qy 1195 CCTGTGGGCTTGCCCCAGCACGTTACCAACCCAGCTGGTGTGAAGAACAGAGGCGTGTAT 1254
 Db 1473 CCCGTGGGCTTGCCCCAGCACGTCACCACCCAGCTGGTGTGCGGAACAAAGGTGTAC 1532
 Qy 1255 GAGAGCGTGAAGTACATCCAGCAGGAGAACCTCTGGATTGGCCCCAGCTCGATTGACCTC 1314
 Db 1533 GAGAGCGTGAAGTACATCCAGCAGGAGAACCTCTGGATTGGCCCCAGCTCGATTGACCTG 1592
 Qy 1315 ATTCACCTGGGAGCAAAGTTCTGCCCTGCATCCGGAAAGGACCAGCAAATTGAGCAGCTG 1374
 Db 1593 ATCCACCTGGGGGCCAAGTTCTCACCCCTGCATCCGGAAAGGACGGGCAGATCGAGCAGCTG 1652
 Qy 1375 GTACGGAGGGAGCGCGACATTGAGCGCACCTCTGGCTGCTGTGTCAGAATGACCGCTCG 1434
 Db 1653 GTGCTGCGCGAGCGAGACCTGGAGCGGGACTCAGGCTGCTGTGTCAGAATGACCACTCC 1712
 Qy 1435 GGCTGCATCCAGACCCCTGAAGAACGGACTGCTGGAGACTTTAGCCACGTTGTAAAGTGG 1494
 Db 1713 GGATGCATCCAGACCCAGCGGAAGGACTGCTGGAGACTTTGCCACTTTGTCAAGTGG 1772
 Qy 1495 CAGAATGATACTGGGCCCTC---AGACAAGTCTGACCTGAGCCAGAACGCCATCGCG 1551
 Db 1773 CAGGATGACACTGGCCCCCATGGACAAGTCTGATCTGGCCAGAACGGACTTCGGGG 1832
 Qy 1552 GTTGTGTGCCACCAAGACCCAGGACCTGTGAAGAGCCTGCCAGTGGGCCACATC 1611
 Db 1833 GCTGTCTGCCACCAGGACCCAGGACCTGCGAGGAGCCAGCCTCCAGCGGTGCCACATC 1892
 Qy 1612 TGGCCTGATGACATTACCAAGTGGCGATCTGCACAGAGCAGGCTCAGAGCAACCACAG 1671
 Db 1893 TGGCCCGATGACATCACTAAGTGGCGATCTGCACAGAGCAGGCCAGGAGCAACCACACA 1952
 Qy 1672 GGCTTGTGCACATAGACTGTAAGATCAAAGGCCCTGCTGCATGGCACCAAGGGC 1731
 Db 1953 GGCTTCCTGCACATGGACTGCGAGATCAAGGGCCCTGCTGCATGGCACCAAGGGC 2012

Qy	1732 AGCTGCGAGATCACCACTCGGGAGTACTGTGAGTCATGCATGGCTATTCCATGAAGAC	1791
Db	2013 AGCTGTGAGATCACCAACCAGGAATACTGTGAGTCATGCACGGCTATTCCATGAGGAA	2072
Qy	1792 GCGACGCTGTGTTCCCAGGTGCACTGTTAGACAAGGTGTGGGCTCCTGCCCTCCTC	1851
Db	2073 GCAACACTCTGCTCCCAGGTGCACTGCTGGACAAGGTGTGGCTGCTGCCCTCCTC	2132
Qy	1852 AACCTGAGGTCCCTGACCAGTTCTACCGATCTGGCTGTCTTATTCCATGCTGGC	1911
Db	2133 AACCTGAGGTCCAGATCAGTTCTACAGGCTCTGGCTGTCTCTCCATGCTGGC	2192
Qy	1912 ATAGTGCACTGCCTTGTGTCGTGGCTTCAAATGACCACCTGAGGGACCTAGAGAAG	1971
Db	2193 GTGGTGCACTGCCTCGTGTCTGTGGCTTCAAATGACCACCTGAGGGACCTGGAGAAG	2252
Qy	1972 CTGGCCGGCTGGCACCGCATCTCATCTTCATCCTTAGTGGCATTACAGGCAACCTG	2031
Db	2253 CTGGCCGGCTGGCACCGTATGCCATCATCTCAGTGGCATTACAGGCAACCTC	2312
Qy	2032 GCCAGCGCCATCTCCTCCCCAACCGGCAGAGGTGGGCCAGCCGGTGCAGTCGGC	2091
Db	2313 GCCAGTGCCATCTTCTCCATACCGGCAGAGGTGGGCCGGCTCACAGTCGGC	2372
Qy	2092 CTCCTCGCCTGCCTCTCGTGGAGCTTCCAGAGCTGGCAGCTGTTGGAGCGGGCTGG	2151
Db	2373 CTCCTCGCCTGCCTCTCGTGGAGCTTCCAGAGCTGGCGCTGCTGGAGAGGCCCTGG	2432
Qy	2152 AAGGCCTTCTTCAACCTGTGGCATTGTGCTTTCCATCTGTGGCCTCTGCC	2211
Db	2433 AAGGCCTTCCCTAACCTCTGGCATTGTGCTCTCCATCTGTGGCCTCTGCC	2492
Qy	2212 TGGATAGACAACATCGCCACATCTTGGGTTCCCTCAGCGCATGCTCTGGCCTCGCC	2271
Db	2493 TGGATCGACAACATCGCCACATCTTGGCTTCCCTCAGTGGCCTGCTGGCCTCGCC	2552
Qy	2272 TTCCCTGCCCTACATTACCTCGGCACCAGCGACAAGTACCGCAAGCGAGCCCTCATCCTC	2331
Db	2553 TTCCCTGCCCTACATCACCTCGGCACCAGCGACAAGTACCGCAAGCGGGACTCATCCTG	2612
Qy	2332 GTGTCGCTGCTGGCTTTGCTGGGCTCTTGCTTCCCTGGCTGTGGCTGTACATCTAC	2391
Db	2613 GTGTCACTGCTGGCTTTGCGCCCTCTCGCCGCCCTCGTGTGGCTGTACATCTAC	2672
Qy	2392 CCCATCAACTGGCCCTGGATCGAGTACCTCACCTGCTTCCCTCACCGCCCTCTGT	2451
Db	2673 CCCATTAACTGGCCCTGGATCGAGCACCTCACCTGCTTCCCTCACCGCCCTCTGC	2732
Qy	2452 GAGAAGTACGAGCTAGACCAGGTGCTACACTAA	2484
Db	2733 GAGAAGTATGAGCTGGACCAGGTGCTGCACTGA	2765

<!--EndFragment-->

SEQ ID NO: 2

<!--StartFragment-->RESULT 3
 ADC42843
 ID ADC42843 standard; protein; 827 AA.
 XX
 AC ADC42843;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE REMAP protein #3.
 XX
 KW Cytostatic; Antiarteriosclerotic; Anti-HIV; Antiinflammatory;
 KW Antiallergic; Antidiabetic; REMAP; pathogenesis.
 XX
 OS Homo sapiens.
 XX
 PN WO2003027228-A2.
 XX
 PD 03-APR-2003.
 XX
 PF 16-JUL-2002; 2002WO-US022833.
 XX
 PR 17-JUL-2001; 2001US-0306020P.
 PR 27-JUL-2001; 2001US-0308179P.
 PR 02-AUG-2001; 2001US-0309702P.
 PR 10-AUG-2001; 2001US-0311476P.
 PR 10-AUG-2001; 2001US-0311551P.
 PR 10-AUG-2001; 2001US-0311718P.
 PR 24-AUG-2001; 2001US-0314798P.
 PR 31-AUG-2001; 2001US-0316639P.
 PR 07-SEP-2001; 2001US-0317996P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Lal PG, Honchell CD, Forsythe IJ, Walia NK, Tang TY, Borowsky ML;
 PI Barroso I, Yue H, Warren BA, Thangavelu K, Gietzen KJ, Azimzai Y;
 PI Lee EA, Baughn MR, Gorvad AE, Duggan BM, Tran B, Li JX;
 PI Richardson TW, Elliott VS, Zebarjadian Y, Tran UK, Yao MG;
 PI Peterson DP, Luo W, Lehr-Mason PM;
 XX
 DR WPI; 2003-421156/39.
 XX
 PT New human receptors and membrane-associated proteins (REMAP), useful for
 PT diagnosing, treating or preventing disorders associated with aberrant
 PT REMAP expression, e.g. cancer, AIDS, atherosclerosis, hypertension or
 PT stroke.
 XX
 PS Claim 1; SEQ ID NO 3; 115pp; English.
 XX
 CC The present invention relates to an isolated polypeptide. The
 CC polypeptides and polynucleotides are useful in diagnosing, treating and
 CC preventing disorders associated with aberrant expression of REMAP, such
 CC as cell proliferative, autoimmune/inflammatory, renal, neurological,
 CC cardiovascular, metabolic, developmental, endocrine, muscle,
 CC gastrointestinal, lipid metabolism or transport disorders, and viral
 CC infections. These are also useful in assessing the effects of exogenous
 CC compounds on the expression of nucleic acids and amino acid sequences of
 CC REMAP, in facilitating drug discovery process, and in investigating the
 CC pathogenesis of diseases or medical conditions. Expression and
 CC purification were achieved using bacterial or virus-based expression
 CC systems. The present sequence represents an REMAP protein of the
 CC invention.

WO 2003027228-A2

XX

SQ Sequence 827 AA;

Query Match 92.1%; Score 4088; DB 7; Length 827;
 Best Local Similarity 91.6%; Pred. No. 0;
 Matches 760; Conservative 31; Mismatches 33; Indels 6; Gaps 4;

Qy	1 MASADKNGSNLPSVSGSRLQSRKPPNLSITIPPP--ESQAPGEQDSMLPERRKNPAYLKS 58 :: :
Db	1 MASADKNGGSVSSVSSRLQSRKPPNLSITIPPPEKETQAPGEQDSMLPE-RKNPAYLKS 59
Qy	59 VSLQEPRGRWQEGAERPGFRRQASLSQSIRKSTAQWFGVSGDWEGKRQNWHRRSLHHCS 118 : :
Db	60 VSLQEPRSRWQESSEKRPGFRRQASLSQSIRKGAAQWFGVSGDWEGQRQQWQRRSLHHCS 119
Qy	119 VHYGRLKASCQRELELPSQEVPFSQGTESPCKPKMPKIVDPLARGRAFRHPDEVDRPHAA 178 : : :
Db	120 MRYGRLKASCQRDLELPSQEAPSFQGTESPCKPKMPKIVDPLARGRAFRHPEEMDRPHAL 179
Qy	179 HPPLTPGVLSLTSFTSVRSGYSHLPRRKRISSVAHMSFQAAAALLKGRSVLDATGQRCRHV 238 :
Db	180 HPPLTPGVLSLTSFTSVRSGYSHLPRRKRMSSVAHMSLQAAAALLKGRSVLDATGQRCRVV 239
Qy	239 KRSFAYPSFLEEDAVDGADTFDSSFFSKEEMSSMPDDVFESPPLSASYFRGVPHSASPVS 298 : : :
Db	240 KRSFAFPSSFLEEDVVDGADTFDSSFFSKEEMSSMPDDVFESPPLSASYFRGIPHHSASPVS 299
Qy	299 PDGVHIPLKEYSGGRALGPQTQRGKRIASKVKHFADRKKRHYGLGVVGWNWLNRSYRSI 358 :
Db	300 PDGVQIPLKEY--GRAPVPGPGRGKRIASKVKHFADRKKRHYGLGVVGWNWLNRSYRSI 357
Qy	359 SSTVQRQLESFDSHRPYFTYWLTFVIIITLLVICTYGIAPVGFAQHVTTQLVLKNRGVY 418 : :
Db	358 SSTVQRQLESFDSHRPYFTYWLTFVIIITLLVICTYGIAPVGFAQHVTTQLVLRNKGVY 417
Qy	419 ESVKYIQQENFWIGPSSIDLILHGAKFSPCIRKDQQIEQLVRERERDIERTSGCCVQNDRS 478 : :
Db	418 ESVKYIQQENFWVGPSIDLIHGAKFSPCIRKDQIEQLVLERDLSGCCVQNDHS 477
Qy	479 GCIQTLKKDCSETLATFVKWQNDTG-PSDKSDLSQLQPSAVVCHQDPRTCEEPASSGAHI 537 : : :
Db	478 GCIQTLKKDCSETLATFVKWQDDTGPPMDKSDLGQKRTSGAVCHQDPRTCEEPASSGAHI 537
Qy	538 WPDDITKWPICTEQAQSNHTGLLHIDCKIKGRPCCIGTKGSCEITTREYCEFMHGYFHD 597 : : :
Db	538 WPDDITKWPICTEQARSNHTGFLHMDCIEIKGRPCCIGTKGSCEITTREYCEFMHGYFHEE 597
Qy	598 ATLCSQVHCLDKVCGLLPFLNPEVPDQFYRIWLSLFLHAGIVHCLVSVVFQMTILRDLEK 657 : :
Db	598 ATLCSQVHCLDKVCGLLPFLNPEVPDQFYRLWLSLFLHAGVVHCLVSVVFQMTILRDLEK 657
Qy	658 LAGWHRISIIFILSGITGNLASAIFLPYRAEVGPAGSQFGLLAclfVELFQSWQLLERPW 717 : : :
Db	658 LAGWHRIAIIIFILSGITGNLASAIFLPYRAEVGPAGSQFGLLAclfVELFQSWPLLERPW 717
Qy	718 KAFFNLSAIVLFLFICGLLPWIDNIAHIFGFLSGMLLAFALPYITFGTSDKYRKRALIL 777 : :
Db	718 KAFLNLSAIVLFLFICGLLPWIDNIAHIFGFLSGLLLAFALPYITFGTSDKYRKRALIL 777
Qy	778 VSLLVFAGLFASLVLWLWIYPINWPWIEYLTCFPFTSRFCEKYELDQVLH 827 : :

Db 778 VSLLAFAGLFAALVLWLYIYPINWPWIEHLTCFPFTSRFCEKYELDQVLH 827

<!--EndFragment-->